



(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MSPrch\_n n.a. - n.a. database search, using Smith-Waterman algorithm  
on: Thu Aug 21 10:07:45 1997; MasPar time 876.69 Seconds  
Tabular output not generated. 894.092 Million cell updates/sec

Title: >US-08-469-637A-1  
Description: (1-1527) from US08469637A.seq  
Perfect Score: 1527  
N.A. Sequence: 1 GCGCCAGCGCGCGCTCCAA.....TTCAACTGAGAAAAAAA 1527  
Comp: 6CGGGCTCGCGCGCGAGGTT.....AAGTGGACCTTTT

Scoring table:

TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 707517 seqs, 25659390 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database:

EST-STS  
9:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8  
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20  
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26  
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32  
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38  
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44  
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50  
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63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68  
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93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98  
99:EST99  
EST-STS-TWO  
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165:EST165 166:EST166 167:EST167 168:EST168 169:EST169  
170:EST170 171:EST171 172:EST172 173:EST173 174:EST174

Statistics: Mean 11.463; Variance 1.911; scale 5.997

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	563	36.9	602	195	AA037313	zc52h03.r1 Soares sen	0.00e+00
2	327	21.4	346	73	H88769	YW23g12.r1 Homo sapie	0.00e+00
3	187	12.2	458	49	HUM366H09B	Human aorta CDNA 5'-e	0.00e+00
4	173	11.3	370	49	HUM345E08B	Human aorta CDNA 5'-e	0.00e+00
5	114	7.5	303	49	HUM365F01B	Human aorta CDNA 5'-e	2.56e-195
6	114	7.5	387	49	HUM366H11B	Human aorta CDNA 5'-e	2.56e-195
7	56	3.7	157	140	C02463	HUMGS0012349, Human G	4.02e-65
8	24	1.6	504	5	T72414	yc72a07.r1 Homo sapie	1.55e-06
9	23	1.5	344	61	H14106	ym62a03.r1 Homo sapie	3.63e-05
10	23	1.5	442	5	T71938	ye07c04.r1 Homo sapie	3.63e-05
11	23	1.5	470	2	T60480	yb95d03.s1 Homo sapie	3.63e-05
12	21	1.4	222	53	R94906	Yq36b08.s1 Homo sapie	1.36e-02
13	21	1.4	222	53	R94906	Yq36b08.s1 Homo sapie	1.36e-02
14	21	1.4	241	44	H37487	15616 Arabidopsis tha	7.51e-04
15	21	1.4	253	129	HSC08E062	H. sapiens partial CD	1.36e-02
16	22	1.4	267	148	W10583	ma38f10.r1 Soares mou	7.51e-04
17	22	1.4	300	183	AA100384	zn46h08.r1 Strategene	7.51e-04
18	22	1.4	325	65	HUM245F10B	Human aorta CDNA 5'-e	1.36e-02
19	21	1.4	325	112	AT93517	ym60h07.s1 Homo sapie	1.36e-02
20	21	1.4	325	112	AT93517	ym60h07.s1 Homo sapie	1.36e-02
21	21	1.4	330	13	R1CC0437A	Yb42d03.r1 Homo sapie	1.36e-02
22	21	1.4	330	13	R1CC0437A	Rice CDNA, partial se	7.51e-04
23	21	1.4	339	88	H65000	yu66d10.s1 Homo sapie	1.36e-02
24	21	1.4	360	164	C14856	Human fetal brain CDN	7.51e-04
25	21	1.4	362	5	T70903	yc49d03.s1 Homo sapie	1.36e-02
26	22	1.4	380	187	AA142684	mg64e05.r1 Soares 2nd	1.36e-02
27	22	1.4	385	180	AA087288	mo11d06.r1 Life Tech	7.51e-04
28	21	1.4	387	109	H8DH3G03	H. sapiens partial CD	1.36e-02
29	21	1.4	395	5	T71079	yc50c04.r1 Homo sapie	1.36e-02
30	21	1.4	406	126	W76826	me73g11.r1 Soares mou	7.51e-04
31	22	1.4	408	41	R27233	yh53a01.r1 Homo sapie	1.36e-02
32	21	1.4	410	6	T74804	yc66d04.r1 Homo sapie	7.51e-04
33	21	1.4	447	184	AA011021	ze34c01.s1 Soares rec	1.36e-02
34	21	1.4	450	131	N68886	TG5T2z39d10.r1 Toxop	1.36e-02
35	22	1.4	453	193	AA164719	zo39f04.s1 Strategene	7.51e-04
36	21	1.4	453	111	N21157	yx47d01.s1 Homo sapie	7.51e-04
37	22	1.4	465	193	AA164056	mt67g06.r1 Soares mou	1.36e-02
38	22	1.4	465	5	T77351	yd7ze10.r1 Homo sapie	7.51e-04
39	21	1.4	472	57	T42477	5740 Arabidopsis thal	7.51e-04
40	21	1.4	472	147	AA003244	mg48g01.r1 Soares mou	1.36e-02
41	21	1.4	478	177	AA061066	mj66h11.r1 Soares mou	1.36e-02
42	22	1.4	490	55	W81931	me33c11.r1 Soares mou	7.51e-04
43	21	1.4	493	15	R1CS1559A	Rice CDNA, partial se	1.36e-02
44	21	1.4	506	94	N38845	Yy80d11.s1 Homo sapie	7.51e-04
45	21	1.4	509	117	W29026	55c10 Human retina CD	7.51e-04
			798	115	W22001	62e8 Human retina CDN	1.36e-02

## ALIGNMENTS

RESULT 1  
LOCUS AA037313 602 bp mRNA EST 25-NOV-1996  
DEFINITION zc52h03.r1 Soares senescent fibroblasts NbHSF Homo sapiens CDNA  
ACCESSION AA037313  
NID clone 325973 5'  
KEYWORDS g1512420  
EST.



DB	121	tgcttcctcmaaatggtcgagatcccaatggatgaagaaactgtttcgaaggaacttgg	180			
QY	1271	TGTTTCTCACAATGGCGAGATCCATGGATGAAGTAACGTGTTTTCAGGCACTTGAGG	1330			
Db	181	cttcacgtgatatactttcctcattaccacagtlactaatlttgccacaggtactaaagaa	240			
QY	1331	CTTTCAGATGATATCTTCTCATTACCGAGTACTAATTTGGCCACAGGTACTAATAAGAA	1390			
Db	241	ctatgagtgtgagaaggaactaaactctctccaataaaccacaatggttaatccaac	300			
QY	1391	CTAAGATGTGGAGAAAGAACTAATCATCTCTCCAAATAAACCCCAATGGTT-ATACCAAC	1449			
Db	301	tgtagactcgatcgatcttactactactgactatgtttccctcctnta	346			
QY	1450	TGTAGATCTGGATCGTATTACTACTG-ACATATATTTTCCCTTATTA	1494			
RESULT	3	HUM366H09B	458 bp	MRNA	EST	29-AUG-1995
IS	1	Human aorta	CDNA 5'-end	GEN-366H09.		
ACCESSION		D63135				
NID		9368050				
KEYWORDS		EST (expressed sequence tag); Human aorta; similar to none (May 29, 1995).				
SOURCE		Homo sapiens (library: Clontech human aorta polyA+ mRNA (#572))				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiinae; Homo. 1 (bases 1 to 458)				
AUTHORS		Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Oaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takachi, A., Takeda, S., Matsumoto, T., Takahashi, E.-I., Hirai, Y., Mekawa, H., Shin, S., and Nakamura, Y.				
TITLE		Unpublished (303)				
JOURNAL		Unpublished (1995)				
COMMENT		Submitted (30-May-1995) to DDBJ by: Tsutomu Fujiwara				
		Otsuka GEN Research Institute				
		Otsuka Pharmaceutical Co., Ltd				
		463-10 Kagasuno Kawanchi-cho				
		Tokushima, Tokushima				
		771-01				
		Japan				
		Phone: 0886-65-2888				
		Fax: 0886-37-1035.				
FEATURES		Location/Qualifiers				
source		1..458				
		/organism="Homo sapiens"				
		/clone.lib="Clontech human aorta polyA+ mRNA (#572)"				
BASE COUNT		157 a	74 c	66 g	161 t	
ORIGIN						
		Query Match 12.2%; Score 187; DB 49; Length 458;				
		Best Local Similarity 99.0%; Pred. No. 0.00e+00;				
		Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Db	1	gtgatattcttctcattaccacagtgactaatlttgccacaggggtactcaagaactatga	60			
QY	1337	GTGATATCTTCTCATTATTCACAGTGACTAATTTTGGCCACAGGGTACTAATAAGAAACTATGA	1396			
Db	61	tgtagaagaaggaactaacatctctcccaataaaccacaatggttaatccaactgcaga	120			
QY	1397	TGTGAGAAAGGAGATACATCTCTCTCCAAATAAACCCCAATGGTTAATCCACTGTGACA	1456			
Db	121	tcgtgactgtatctactgactatattttcccttattactgcttcagtaattcaactg	180			
QY	1457	TCTGATACGTATATCTACTGACTATATTTTCCCTTATTACTGCTTCGAGTAATTCACATG	1516			
Db	181	aatataaaaaa	191			
QY	1517	AAAAAAAAAAAA	1527			

RESULT	4	HUM345E08B	370 bp	MRNA	EST	29-AUG-1995
LOCUS		Human aorta cDNA 5'-end	GEN=345E08.			
DEFINITION		D62967				
ACCESSION		g966741				
NID		EST(expressed sequence tag); Human aorta; similar to none(May 29,1995).				
KEYWORDS		Human sapiens (library: Clontech human aorta polyA+ mRNA (#5572))				
SOURCE		cDNA to mRNA.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS		1 (bases 1 to 370) Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Oaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takachi,A., Takeda,S., Matsumae,T., Takahashi,E.-I., Hiral,Y., Makawa,H., Shin,S. and Nakamura,Y.				
TITLE		Unpublished(303)				
JOURNAL		Submitted (30-May-1995) to DDBJ by:				
COMMENT		Rutomu Fujiwara Otsuka GEN Research Institute Otsuka Pharmaceutical Co.,Ltd 463-10 Kagasuno Kawanchi-cho Tokushima, Tokushima 771-01 Japan Phone: 0886-65-2888 Fax : 0886-37-1035. Location/Qualifiers				
FEATURES		Source	1..370	/organism="Homo sapiens"		
				/clone_lib="Clontech human aorta polyA+ mRNA (#5572)"		
BASE COUNT		122 a	63 c	55 g	127 t	3 others
ORIGIN						
Query Match		11.3%; Score 173;	DB 49;	Length 370;		
Best Local Similarity		97.9%;	Pred. No. 0.00e+00;			
Matches 187;		Conservative	0;	Mismatches 2;	Indels 2;	Gaps 2;
Db	1	gtgatcatttcctattaccacgaagactatitggccagaagggtacctaaagaactatga	60			
Oy	1337	GTGATATTCTTTCATCATCCAGTGACTAAATTGGCCACAGGGTACTAAAAGAACAATCATGA	1396			
Db	61	tgttgagaagaagactaacatctcccacaataaacccccaaatggttaatccaactgcaga	120			
Oy	1397	TGTGAGAAAGGAAGATAACATCTCCTCCAATAAACCCCAATGGTTATATCCAACTGCAGA	1456			
Db	121	t-tgatcgattatctactgactatatttcc-ttattactgcttcagtaattcaactg	178			
Oy	1457	TCTGATCGATTACTACTGACTATATTTCCTTTACTTACTGCTTGCAGTAATTCACACTGG	1516			
Db	179	aactaaaaa	189			
Oy	1517	AAAAA	1527			
RESULT	5	HUM365F01B	303 bp	MRNA	EST	29-AUG-1995
LOCUS		Human aorta cDNA 5'-end	GEN=365F01.			
DEFINITION		D63118				
ACCESSION		g968043				
NID		EST(expressed sequence tag); Human aorta; similar to none(May 29,1995).				
KEYWORDS		Human sapiens (library: Clontech human aorta polyA+ mRNA (#6572))				
SOURCE		cDNA to mRNA.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS		1 (bases 1 to 303) Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,				

Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,  
Takachi, A., Takeda, S., Watanabe, T., Takahashi, E.-I., Hirai, Y.,  
Mekawa, H., Shin, S. and Nakamura, Y.  
Unpublished (303)  
Submitted (30-May-1995) to DDBJ by:  
Tsutomu Fujiwara  
Otsuka GEN Research Institute  
Otsuka Pharmaceutical Co., Ltd  
463-10 Kagasuno Kawauchi-cho  
Tokushima, Tokushima  
771-01  
Japan  
Phone: 0886-65-2888  
Fax: 0886-37-1035.  
Location/Qualifiers

FEATURES  
Source  
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/clone\_lib="Clontech human aorta polyA+ mRNA (#6572)"

COUNT 102 a 54 c 37 g 106 t 4 others  
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Best Local Similarity 98.3%; Pred. No. 2,566-195;  
Matches 116; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 ctacacatctctccaaataaaccgaatggtatccacgtcagatcgtgattat 60  
|||  
QY 1410 CTACACATCTCTCCAAATAAACCCCAAGGTATCCAACTGACAGATCGATCGTTAT 1469  
|||  
QY 1470 CTACTGACTATATTTTCCCTTATTACTCTTGACAGTATTAAGTGAAGAAAAA 1527  
|||

RESULT 6  
LOCUS HUM366H1B 387 bp mRNA EST 29-AUG-1995  
DEFINITION Human aorta cDNA 5'-end GEN:566H1.  
ACCESSION D63126  
NID 9688051  
KEYWORDS EST(expressed sequence tag); Human aorta; similar to none(May 29,1995).  
SOURCE Homo sapiens (library: Clontech human aorta polyA+ mRNA (#6572))  
ORGANISM Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 387)  
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,  
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,  
Takachi, A., Takeda, S., Watanabe, T., Takahashi, E.-I., Hirai, Y.,  
Mekawa, H., Shin, S. and Nakamura, Y.  
Unpublished (303)  
Submitted (30-May-1995) to DDBJ by:  
Tsutomu Fujiwara  
Otsuka GEN Research Institute  
Otsuka Pharmaceutical Co., Ltd  
463-10 Kagasuno Kawauchi-cho  
Tokushima, Tokushima  
771-01  
Japan  
Phone: 0886-65-2888  
Fax: 0886-37-1035.  
Location/Qualifiers

TITLE  
JOURNAL  
COMMENT

1..387  
/organism="Homo sapiens"  
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FEATURES  
Source  
1..387  
Location/Qualifiers

BASE COUNT 135 a 62 c 50 g 140 t  
ORIGIN  
Query Match 7.5%; Score 114; DB 49; Length 387;  
Best Local Similarity 98.3%; Pred. No. 2,566-195;

Matches 116; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 ctacacatctctccaaataaaccgaatggtatccacgtcagatcgtgattat 60  
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QY 1410 CTACACATCTCTCCAAATAAACCCCAAGGTATCCAACTGACAGATCGATCGTTAT 1469  
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Db 61 ctactgactatatttcccttactactgcttcagatgaattcaactggaattaaaaa 118  
|||  
QY 1470 CTACTGACTATATTTTCCCTTATTACTCTTGACAGTATTAAGTGAAGAAAAA 1527  
|||

RESULT 7  
LOCUS C02463 157 bp DNA EST 11-JUL-1996  
DEFINITION HUMGS0012349, Human gene signature, 3'-directed cDNA sequence.  
ACCESSION C02463  
NID g1434693  
KEYWORDS Gene Signature; GS; EST(expressed sequence tag); BodyMap; gene expression.  
SOURCE One or more human adult tissue.  
ORGANISM Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 157)  
Direct Submission  
Submitted (28-DEC-1995) to the DDBJ/EMBL/GenBank databases. Kousaku Okubo, Osaka University, Institute for Molecular and Cellular Bio; 1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan  
(E-mail:kousaku@imcb.osaka-u.ac.jp, Tel:06-877-5111(ex.3315), Fax:06-877-1922)  
2 (bases 1 to 157)  
Okubo, K.  
BodyMap: human gene expression database  
Unpublished (1995)  
We are not submitting the same cDNA sequence redundantly to DDBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also found there.  
Location/Qualifiers

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished (1995)  
We are not submitting the same cDNA sequence redundantly to DDBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also found there.

FEATURES  
Source  
1..157  
/organism="Homo sapiens"

BASE COUNT 46 a 26 c 24 g 54 t 7 others  
ORIGIN

Query Match 3.7%; Score 56; DB 140; Length 157;  
Best Local Similarity 95.5%; Pred. No. 4,026-65;  
Matches 64; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Db 1 gatcgtatctactgactatatttccctgattactgcttcagatgaattcaactgga 60  
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QY 1461 GATCGTATCTACTGACTATATTTTCCCT-TATTACTGCTTGACAGTATTAATCACTGAAA 1519  
|||  
Db 61 ttaaaa 67  
|||  
QY 1520 AAAAAA 1526

RESULT 8  
LOCUS T72414 504 bp mRNA EST 01-MAR-1995  
DEFINITION YC72407 r1 Homo sapiens cDNA clone 86196 5' similar to  
9D:X54486\_fnal PLASMA PROTEASE C1 INHIBITOR PRECURSOR (HUMAN);  
ACCESSION T72414  
NID 9686935  
KEYWORDS EST.  
SOURCE human clone=86196 library=Stratagene liver (#937224)  
vector=pBluescript SK host=30R cells (kanamycin resistant)  
primer-M13P1 Rsite1-EcoRI Rsite2-XhoI Cloned unidirectionally.  
Primer: Oligo dT. Hepatectomy from normal 49 year old male  
caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; 5'  
adaptor sequence: 5'-GAATTCGCGACGAG-3'; 3' adaptor sequence:  
5'-CTCGAGTTTCTTTTCTTTTCTTTT-3'.



## ORIGIN

Query Match 1.5%; Score 23; DB 5; Length 442;

Best Local Similarity 79.5%; Pred. No. 3.63e-05;

Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 332 agcacatgggaacagggttccaggcccttcttctttt 370

Cp 1022 AGGATCTGGTCACTGGGTTGCATGCTTATTTGTTT 984

## RESULT 11

LOCUS T60480 470 bp mRNA EST 13-FEB-1995

DEFINITION YB55d03.s1 Homo sapiens cDNA clone 78917 3' similar to gp:X04225

ACCESSION T60480

KEYWORDS T60480

SOURCE EST.

human clone-78917 library-Stratagene liver (#937224)  
vector-pBluescript SK host-SOBR cells (kanamycin resistant)  
primer-21m3 Rstet-EcoRI Rstet2-XhoI cloned unidirectionally.  
Primer: Oligo dt Hepatectomy from normal 49 year old male  
Caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector: 5'  
adaptor sequence: 5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:  
5'-CTCGAGTCTTTTCTTTTCTTTT-3'.

ORGANISM Homo sapiens

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 470)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaekis,E.,

Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

WashU-Merck EST Project

Unpublished (1995)

TITLE JOURNAL

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 374

Source: IMAGE Consortium, LNL.

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

LOCATION/Qualifiers

1..470

Source

Base Count

95 a 137 c 125 g 108 t 5 others

ORIGIN

Query Match

Best Local Similarity 72.3%; Pred. No. 3.63e-05;

Matches 34; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 407 ccatggatgacccattnttagaataaccctgctgctcattcc 453

Cp 1300 CCATGGATCTGCCAATGTGAGGAACAGCTCATGCGCATTTCC 1254

## RESULT 12

LOCUS R94906 222 bp mRNA EST 31-AUG-1995

DEFINITION YG39B08.s1 Homo sapiens cDNA clone 198135 3'.

ACCESSION R94906

KEYWORDS 9973636

SOURCE EST.

human clone-198135 primer-Bromega -21m3 library-Soares fetal liver  
spleen INRS vector-p7713D (Pharmacia) with a modified polylinker  
host-BH10B (ampicillin resistant) Rstet-Eco RI liver  
and spleen from a 20 week-post conception male fetus. 1st strand

## ORGANISM

cDNA was primed with a Pac I - Oligo(dt) primer [5'  
AACTGAGAGAAATTAATTAAGACATCTTTTCTTTTCTTTT 3'], double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac  
I and cloned into the Pac I and Eco RI sites of the modified p7713  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M.Patila Bonaldi.

Homo sapiens

Eucaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 222)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaekis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson,R.

The WashU-Merck EST Project

Unpublished (1995)

TITLE JOURNAL

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 201

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

LOCATION/Qualifiers

1..222

Source

Base Count

31 a 84 c 1 g 77 t 29 others

ORIGIN

Query Match

Best Local Similarity 60.0%; Pred. No. 1.36e-02;

Matches 33; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Db 131 ttttccttttaattccttcttcaantcttcnaacnaaatccct 185

Cp 994 TTATGTTTTCATGCTTCTGCTCCACTTCTTCCGGTAAGCTTCCAT 940

## RESULT 13

LOCUS H37487 241 bp mRNA EST 25-JUL-1995

DEFINITION 15616 Arabidopsis thaliana cDNA clone 182E107.

ACCESSION H37487

KEYWORDS 9906986

SOURCE EST.

The cress clone-182E107 library-Lambda-PR2 strain-var columbia  
vector-lambda zip-lox primer-T7 dye primer Rstet-Sal Rstet2-Not  
Lambda PR2 is a cDNA library derived from equal quantities of 4  
pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated  
seedlings; 2) tissue culture grown roots; 3) staged plants half  
with 24 hour light cycle, half on 16 hr light, 8 hour dark-  
rosettes; 4) same plants as 3 but aerial tissue (stems, flowers  
and siliques). The vector is BRL's lambda zip-lox. The cDNA  
inserts were directionally cloned with Sal-Not arms using oligo dt  
primed cDNA.

ORGANISM Arabidopsis thaliana

Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Caprales;

Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 241)

AUTHORS Newman,T., de Bruijn,F.J., Green,P., Keegstra,K., Kende,H.,

McIntosh,L., Ohlrogge,J., Raikhe,N., Somerville,S., Thomashow,M.,

Reitel,E. and Somerville,C.

Genes galore: a summary of methods for accessing results from  
large-scale partial sequencing of anonymous Arabidopsis cDNA clones

JOURNAL Plant Physiol. 106, 1241-1255 (1994)  
 COMMENT  
 Contact: Thomas Newman  
 MSU-DOE Plant Research Laboratory  
 Michigan State University  
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg. E,  
 Lansing, MI  
 Tel: 517-353-0854  
 Fax: 517-353-9168  
 Email: 22133cne@bm.cl.msu.edu.  
 Location/Qualifiers  
 1..241  
 /organism="Arabidopsis thaliana"  
 /clone="182E107"  
 /strain="var Columbia"  
 BASE COUNT 72 a 41 c 50 g 70 t 8 others  
 ORIGIN  
 Query Match 1.4%; Score 22; DB 44; Length 241;  
 Local Similarity 74.4%; Pred. No. 7.51e-04;  
 Matches 32; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
 Db 32 aaaaataatcagaagaagatcatgcatgcatatgtat 74  
 Cp 1485 AAAATATAGTCAGTACATACCATCTCAGATCTGCACATTGGAT 1443  
 RESULT 14  
 LOCUS HSC0B062 253 bp RNA EST 21-SEP-1995  
 DEFINITION H. sapiens partial cDNA sequence; clone c-0be06.  
 ACCESSION Z38433  
 MID 9360441  
 KEYWORDS partial cDNA sequence; transcribed sequence fragment.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrate; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS 1 (bases 1 to 253)  
 TITLE Genexpress.  
 JOURNAL Direct Submission  
 Submitted (24-OCT-1994) Genethon, B.P. 60, 91002 Evry Cedex France  
 and Genetique Moleculaire et Biologie du developpement, CNRS UPR422  
 B.P. 8, 94801 Villejuif Cedex France. E-mail: genexpress@genethon.fr  
 2 (bases 1 to 253)  
 REFERENCE Genexpress.  
 AUTHORS The Genexpress cDNA program  
 TITLE unpublished  
 JOURNAL 3 (bases 1 to 253)  
 AUTHORS Aufferay, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,  
 Drenth, M.D., Duprat, S., Houlgate, R., Juneau, M.N., Lamy, B.,  
 Lorenzo, F., Mitchell, H., Marigae-Samson, R., Pilet, G., Pouillot, Y.,  
 Sebastien-Kabatchis, C. and Tessier, A.  
 IMAGE: molecular integration of the analysis of the human genome  
 and its expression  
 C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)  
 95277534  
 JOURNAL Clone library from B. Soares, Psychiatry Dept. Columbia University  
 MEDLINE  
 COMMENT  
 USA:  
 Cloning\_method: total mRNA was oligo-(dT) primed and directionally  
 cloned 5' -> 3' into the HindIII -> NotI sites of the latmid BA  
 vector;  
 Sequencing\_method: single read, full automatic;  
 Primer: (-21)M13 universal;  
 cDNA sequence complementary to mRNA (3'end)  
 Stretch\_removed: 31 T removed at sequence 5'end  
 Normalization\_method: Bento Soares, P.N.A.S in press;  
 Genexpress\_library\_idt: C;  
 Genexpress\_sequence\_idt: a1c-0be06;  
 No significant homology found with:  
 genbank release 81 swissprot release 28.  
 Location/Qualifiers

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SOURCE
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/organism="Homo sapiens"
/isolate="muscular atrophy patient"
/dev_stage="3 months old"
/tissue_type="total brain"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
BASE COUNT      76 a       57 c       49 g       70 t       1 others
ORIGIN

Query Match          1.4%   Score 21; DB 129; Length 253;
Best Local Similarity 78.4%; Pred. No. 1,35e-02;
Matches    29; Conservative    0; Mismatches    8; Indels    0; Gaps    0;

Db    123 acacagctcacatgttacagacaataaacctgcctaag 159
      ||||| | | | | | | | | | | | | | | | | | | | |
Oy    774 ACACAGCTCACACAGAACAGACTTTCACACTCCTGTAAG 810

RESULT    15
LOCUS     W10583                267 bp      mRNA           EST            05-SEP-1996
DEFINITION mas8f10.r1 Soares mouse pJNMF19.5 Mus musculus cDNA clone 313003 5'
similar to gb:219554 VIMENTIN (HUMAN);.
ACCESSION W10583
NID        91284900
KEYWORDS   house mouse.
SOURCE     Mus musculus
ORGANISM   Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE 1 (bases 1 to 267)
AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gesel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE      The WashU-HMHI Mouse EST Project
JOURNAL    Unpublished (1996)
COMMENT    Contact: Marra M/Mouse EST Project
WashU-HMHI Mouse EST Project
Washington University School of Medicine#
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
Seq primer: EMPprimer.
Location/Qualifiers
1..267
/organism="Mus musculus"
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polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCATCTCAAGCGGAGGGCCGCATTCTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pUT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5 library constructed by Bento
Soares and M.Fatima Bonaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."
/clone="313003"
/clone_lib="Soares mouse pJNMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
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MRNA
BASE COUNT      78 a       70 c       61 g       58 t
ORIGIN

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Query Match 1.4%; Score 22; DB 148; Length 267;  
 Best local Similarity 75.0%; Pred. No. 7.51e-04;  
 Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
 Db 31 gaagctgctggaagcgagagacatgattctctgctctgc 74  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Cp 931 GAAGCTGCTCGAAGTGAGCTAGCATGTCCAAATGTGCGCTGC 888

Search completed: Thu Aug 21 10:35:06 1997  
 Job time : 1641 secs.